# **Special Issue**

## Global Analysis of Tracking the Evolution of SARS-CoV-2 Variants

### Message from the Guest Editor

SARS-CoV-2, a positive-sense \( \Brightarrow\)-coronavirus, is the etiological agent of COVID-19. Although it possesses an error-prone viral RNA-dependent RNA polymerase with limited 3'-5' exoribonuclease activity, it can cause progeny viruses with new mutations, affecting its infectivity, transmissibility, and virulence. Moreover, recently, a sharp decline in PCR testing due to high cost and reliance on antigen testing kits could lead to the potential underreporting of new emerging variants. Therefore, the continuous monitoring and tracking of new variants on a globe scale, as well as the characterization of mutations, is crucial because of their effect on adaptive immunity, neutralizing antibody response, and impact on vaccine efficacy. The detailed maps of mutations highlighting their prospective role in therapeutics and vaccine development can better prepare us for future waves of continuously evolving SARS-CoV-2. With this aim, we invite original research and review articles which address the tracking and genomic surveillance of emerging variants, their virulence, transmissibility, mathematical modeling, and therapeutic aspects of COVID-19.

#### **Guest Editor**

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## Deadline for manuscript submissions

closed (30 June 2023)



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Vaccines (ISSN 2076-393X) has had a 6-year history of publishing peer-reviewed state of the art research that advances the knowledge of immunology in human disease protection. Immunotherapeutics, prophylactic vaccines, immunomodulators, adjuvants and the global differences in regulatory affairs are some of the highlights of the research published that have shaped global health. Our open access policy allows all researchers and interested parties to immediately scrutinize the rigorous evidence our publications have to offer. We are proud to present the work and perspectives of many to contribute to future decisions concerning human health.

#### Editor-in-Chief

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